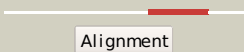

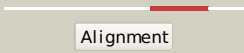







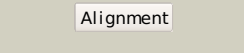

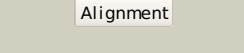

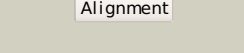



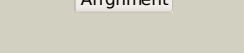

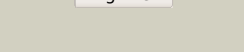






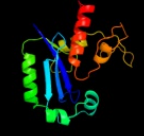



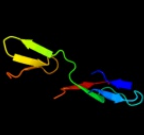


Phyre2

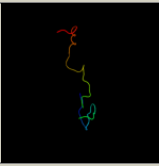

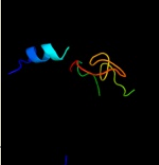

Email	l.a.kelley@imperial.ac.uk
Description	A0PJM3
Date	Tue Apr 3 14:51:25 BST 2012
Unique Job ID	c4985a30697b406b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wlja_	 Alignment		99.9	35	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
2	d2guia1	 Alignment		99.7	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
3	d2igia1	 Alignment		99.6	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
4	dlj9aa_	 Alignment		99.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
5	c2pljB_	 Alignment		99.5	21	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii polc-type; PDBTitle: crystal structure of a polc-type dna polymerase iii2 exonuclease domain from thermotoga maritima
6	c2gbzA_	 Alignment		99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix
7	c3tr8A_	 Alignment		99.5	20	PDB header: hydrolase Chain: A: PDB Molecule: oligoribonuclease; PDBTitle: structure of an oligoribonuclease (orn) from coxiella burnetii
8	c3cm6A_	 Alignment		99.5	14	PDB header: hydrolase, apoptosis Chain: A: PDB Molecule: cell death-related nuclease 4; PDBTitle: crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er
9	d1w0ha_	 Alignment		99.5	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
10	c1zbbA_	 Alignment		99.5	16	PDB header: hydrolase/rna Chain: A: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease
11	c2xriA_	 Alignment		99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: eri1 exoribonuclease 3; PDBTitle: crystal structure of human eri1 exoribonuclease 3

12	d1y97a1	Alignment		99.4	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
13	d2f96a1	Alignment		99.3	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
14	c3u6fA_	Alignment		99.3	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: three prime repair exonuclease 1; PDBTitle: mouse trex1 d200n mutant
15	d3b6oa1	Alignment		99.3	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
16	c1zbuB_	Alignment		99.3	16	PDB header: hydrolase Chain: B: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: crystal structure of full-length 3'-exonuclease
17	d2qxfa1	Alignment		99.2	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
18	c2is3B_	Alignment		98.6	16	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease t; PDBTitle: crystal structure of escherichia coli rnase t
19	d1kfsa1	Alignment		98.3	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
20	c2e6mA_	Alignment		98.3	16	PDB header: hydrolase Chain: A: PDB Molecule: werner syndrome atp-dependent helicase homolog; PDBTitle: structure of mouse werner exonuclease domain
21	c1yt3A_	Alignment	not modelled	98.2	19	PDB header: hydrolase,translation Chain: A: PDB Molecule: ribonuclease d; PDBTitle: crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
22	c2kzZA_	Alignment	not modelled	98.2	18	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: klenow fragment with normal substrate and zinc only
23	d1yt3a3	Alignment	not modelled	97.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
24	c2xcmE_	Alignment		97.5	21	PDB header: chaperone/protein binding Chain: E: PDB Molecule: rar1; PDBTitle: complex of hsp90 n-terminal, sgt1 cs and rar1 chord2 domain
25	d2hbka2	Alignment	not modelled	97.5	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
26	c3cymA_	Alignment	not modelled	97.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
27	c2hbka_	Alignment	not modelled	97.4	22	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the yeast nuclear exosome component, rrp6p,2 reveals an interplay between the active site and the hrdc3 domain; protein in complex with mn

28	d1uoca_	Alignment	not modelled	97.3	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF 1-like ribonuclease
29	c2yrtA_	Alignment		97.2	27	PDB header: transcription Chain: A: PDB Molecule: chord containing protein-1; PDBTitle: solution structure of the chord domain of human chord-2 containing protein 1
30	c1njzA_	Alignment	not modelled	97.1	16	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase i; PDBTitle: cytosine-thymine mismatch at the polymerase active site
31	c3sahA_	Alignment	not modelled	97.1	21	PDB header: hydrolase Chain: A: PDB Molecule: exosome component 10; PDBTitle: crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site
32	d1vk0a_	Alignment	not modelled	97.1	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
33	d2d5ra1	Alignment	not modelled	97.0	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: CAF 1-like ribonuclease
34	c2p51A_	Alignment	not modelled	97.0	17	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: spcc18.06c protein; PDBTitle: crystal structure of the s. pombe pop2p deadenylation2 subunit
35	d2hhva1	Alignment	not modelled	96.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
36	d1wn7a1	Alignment	not modelled	96.4	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
37	d1tgoa1	Alignment	not modelled	95.9	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
38	c2k0nA_	Alignment		95.3	11	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription PDBTitle: solution structure of yeast gal11p kix domain
39	d1qhta1	Alignment	not modelled	95.0	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
40	c4ktqA_	Alignment	not modelled	94.8	17	PDB header: transferase/dna Chain: A: PDB Molecule: protein (large fragment of dna polymerase i); PDBTitle: binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
41	d1d5aa1	Alignment	not modelled	94.5	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
42	c1q8iA_	Alignment	not modelled	94.3	19	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii; PDBTitle: crystal structure of escherichia coli dna polymerase ii
43	d1q8ia1	Alignment	not modelled	94.0	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
44	c2dtuA_	Alignment	not modelled	93.7	19	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the beta hairpin loop deletion variant2 of rb69 gp43 in complex with dna containing an abasic site3 analog
45	c1s5jA_	Alignment	not modelled	93.1	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus
46	d1ih7a1	Alignment	not modelled	92.3	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
47	c3iayA_	Alignment	not modelled	91.4	21	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
48	c1tk0A_	Alignment	not modelled	91.0	15	PDB header: transferase/electron transport/dna Chain: A: PDB Molecule: dna polymerase; PDBTitle: t7 dna polymerase ternary complex with 8 oxo guanosine and2 ddc2p at the insertion site
49	c2a1sC_	Alignment	not modelled	89.5	17	PDB header: hydrolase Chain: C: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of native parn nuclease domain
50	d1s5ja1	Alignment	not modelled	89.3	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
51	c1d5aA_	Alignment	not modelled	88.9	19	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase); PDBTitle: crystal structure of an archaeobacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
52	c3d45B_	Alignment	not modelled	86.4	15	PDB header: hydrolase Chain: B: PDB Molecule: poly(a)-specific ribonuclease parn;

						PDBTitle: crystal structure of mouse parn in complex with m7gpppg
53	d1noya_	Alignment	not modelled	86.3	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
54	c2ys2A_	Alignment	not modelled	84.9	25	PDB header: transferase Chain: A: PDB Molecule: cytoplasmic tyrosine-protein kinase bmx; PDBTitle: solution structure of the btk motif of human cytoplasmic2 tyrosine-protein kinase bmx
55	d1x9ma1	Alignment	not modelled	84.4	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
56	c2e6iA_	Alignment		84.2	15	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase itk/tsk; PDBTitle: solution structure of the btk motif of tyrosine-protein2 kinase itk from human
57	d1btka_	Alignment	not modelled	82.5	34	Fold: PH domain-like barrel Superfamily: PH domain-like Family: PIeckstrin-homology domain (PH domain)
58	c2vwkA_	Alignment	not modelled	82.0	18	PDB header: dna replication Chain: A: PDB Molecule: dna polymerase; PDBTitle: uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
59	c2gv9B_	Alignment	not modelled	81.9	13	PDB header: transferase Chain: B: PDB Molecule: dna polymerase; PDBTitle: crystal structure of the herpes simplex virus type 1 dna polymerase
60	cli6vD_	Alignment		78.7	31	PDB header: transcription Chain: D: PDB Molecule: dna-directed rna polymerase; PDBTitle: thermus aquaticus core rna polymerase-rifampicin complex
61	dli6vd_	Alignment		78.7	31	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
62	d1ynjd1	Alignment		76.4	29	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
63	c1cmwA_	Alignment	not modelled	74.5	18	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
64	c2gutA_	Alignment	not modelled	74.3	12	PDB header: transcription Chain: A: PDB Molecule: arc/mediator, positive cofactor 2 glutamine/q- PDBTitle: solution structure of the trans-activation domain of the2 human co-activator arc105
65	c3bdvB_	Alignment	not modelled	60.2	35	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
66	d3bzka5	Alignment	not modelled	56.7	27	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
67	c3ho6B_	Alignment	not modelled	53.1	16	PDB header: toxin Chain: B: PDB Molecule: toxin a; PDBTitle: structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
68	c3qqcA_	Alignment	not modelled	51.2	18	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit b, dna-directed rna PDBTitle: crystal structure of archaeal spt4/5 bound to the rnap clamp domain
69	c3zyqA_	Alignment	not modelled	48.2	14	PDB header: signaling Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
70	d1wiga2	Alignment	not modelled	45.8	21	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
71	c1dvpA_	Alignment	not modelled	42.4	18	PDB header: transferase Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
72	c1pqvS_	Alignment	not modelled	40.0	15	PDB header: transferase/transcription Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis complex
						PDB header: transferase/transcription/dna-rna hybrid

73	c1y1yS_	Alignment	not modelled	40.0	15	Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis-dna/rna complex
74	d1wfla_	Alignment	not modelled	38.8	26	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
75	c2kvfA_	Alignment	not modelled	37.8	30	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
76	d1sb0a_	Alignment	not modelled	34.5	11	Fold: Kix domain of CBP (creb binding protein) Superfamily: Kix domain of CBP (creb binding protein) Family: Kix domain of CBP (creb binding protein)
77	c3hz6A_	Alignment	not modelled	33.1	16	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
78	c2e72A_	Alignment	not modelled	32.8	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pogo transposable element with znf domain; PDBTitle: solution structure of the zinc finger domain of human2 kiaa0461
79	d1libia1	Alignment	not modelled	32.4	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
80	c2cftA_	Alignment	not modelled	32.2	15	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
81	d1g47a1	Alignment	not modelled	31.5	32	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
82	d1gpla2	Alignment	not modelled	31.4	34	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
83	d1x6ha1	Alignment	not modelled	30.2	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
84	c3psfA_	Alignment	not modelled	29.8	18	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
85	c2elrA_	Alignment	not modelled	28.7	19	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406
86	c2akIA_	Alignment	not modelled	27.5	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
87	c2jr7A_	Alignment	not modelled	27.1	16	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
88	d2k4xa1	Alignment	not modelled	27.1	21	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
89	c2lo3A_	Alignment	not modelled	26.2	23	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 73; PDBTitle: solution structure of sgf73(59-102) zinc finger domain
90	c2zkr4_	Alignment	not modelled	25.8	23	PDB header: ribosomal protein/rna Chain: 4: PDB Molecule: 60s ribosomal protein 144e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
91	c2f9yB_	Alignment	not modelled	25.7	16	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
92	d2f9yb1	Alignment	not modelled	25.7	16	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
93	d1ubdc2	Alignment	not modelled	24.2	40	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
94	d1b8ta3	Alignment	not modelled	23.8	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
95	c3lp5A_	Alignment	not modelled	23.2	12	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
96	d1pjaa_	Alignment	not modelled	23.1	8	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
97	c1pjaA_	Alignment	not modelled	23.1	8	PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
98	d2b4jc1	Alignment	not modelled	22.9	15	Fold: N-cbl like Superfamily: HIV integrase-binding domain

						Family: HIV integrase-binding domain
99	d1jvna1	Alignment	not modelled	22.8	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
100	d1uxoa_	Alignment	not modelled	22.5	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
101	c2gb5B_	Alignment	not modelled	22.4	23	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
102	d2b0la1	Alignment	not modelled	22.2	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cody HTH domain
103	c1t39A_	Alignment	not modelled	21.9	22	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
104	c2co8A_	Alignment	not modelled	21.6	23	PDB header: metal binding protein Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: solution structures of the lim domain of human nedd92 interacting protein with calponin homology and lim domains
105	d1ywsa1	Alignment	not modelled	21.3	16	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
106	c2zyiB_	Alignment	not modelled	21.2	28	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
107	d1xpa2	Alignment	not modelled	20.8	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain
108	d1ydfa1	Alignment	not modelled	20.6	11	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
109	d2yt9a1	Alignment	not modelled	20.4	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
110	c2k42A_	Alignment	not modelled	20.2	21	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protein; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehcc effector
111	c1b8tA_	Alignment	not modelled	20.1	16	PDB header: contractile Chain: A: PDB Molecule: protein (crp1); PDBTitle: solution structure of the chicken crp1
112	d1wgea1	Alignment	not modelled	20.1	16	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger